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A M E N D M E N T S

Please amend the subject application as set forth below.

In the Claims

Add the following new claims 96 through 105 inclusive. Pursuant to 37 CFR 1.121, a complete listing of all the claims of the subject application is set out below.

Claims 1 – 50 (cancelled without prejudice)

51. (previously added and amended) A method according to claim 72, wherein the reaction values are measurements of an optical signal or a digital image intensity value.

52. (previously added and amended) A method according to claim 74, wherein the reaction values are measurements of an optical signal or a digital image intensity value.

53. (previously added) A method according to claim 51, wherein the optical signal is an optical density.

54. (previously added) A method according to claim 52, wherein the optical signal is an optical density.

Claim 55 (cancelled without prejudice)

56. (previously added and amended) A method according to claim 72, wherein the reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, hybridization, allele-specific amplification and a ligase chain reaction.

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57. (previously added) A method according to claim 56, wherein the reaction values are obtained by assaying for alleles using genetic bit analysis.

58. (previously added and amended) A method according to claim 74, wherein the reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, hybridization, allele-specific amplification and a ligase chain reaction.

59. (previously added) A method according to claim 58, wherein the reaction values are obtained by assaying for alleles using genetic bit analysis.

60. (previously added and amended) A method according to claim 72, further comprising detecting the presence of a downward trend in confidence scores over time.

61. (previously added) A method according to claim 60, further comprising triggering an alarm condition upon detecting a statistically significant downward trend in confidence scores over time.

62. (previously added and amended) A method according to claim 72, wherein the reaction values are obtained by assaying for one or more alleles that provide information relating to a trait.

63. (previously added and amended) A method according to claim 74, wherein the reaction values are obtained by assaying for one or more alleles that provide information relating to a trait.

64. (previously added and amended) A method according to claim 72, wherein one or more of the reaction values are obtained by assaying for one or more alleles that provide information pertaining to parentage of the subject.

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65. (previously added and amended) A method according to claim 74, wherein one or more of the reaction values are obtained by assaying for one or more alleles that provide information pertaining to parentage of the subject.

66. (previously added and amended) A method according to claim 72, wherein more than one genetic loci are analyzed.

67. (previously added and amended) A method according to claim 72, wherein the reaction values are obtained by assaying for one or more alleles that provide information useful for determining the identity of the subject.

68. (previously added and amended) A method according to claim 74, wherein the reaction values are obtained by assaying for one or more alleles that provide information useful for determining the identity of the subject.

69. (previously added) A method of determining for a plurality of samples analyzed with comparable biochemistry a genotype and confidence score for the genotype at a locus within genetic material, comprising:

(a) measuring, under comparable conditions, a first reaction value for each sample, indicative of the presence of a given allele at the locus;

(b) forming a data set from the reaction values;

(c) establishing initial probability distributions for the genotype of interest at the locus;

(d) calculating the conditional probability of each genotype of interest at the locus by applying the first reaction value to each probability distribution in the set of probability distributions that corresponds to the first reaction value; and

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(e) determining the genotype and confidence score.

70. (previously added) A method according to claim 69, further comprising:

measuring, under comparable biochemistry, a second reaction value corresponding to the presence of a second allele at the locus;

forming a data set of reaction values corresponding to the second allele;

applying the first and second reaction values to each pertinent probability distribution to determine a measure of the conditional probability of each genotype of interest at the locus, and

determining the confidence score and genotype for each sample.

71. (previously added) A method according to claims 69 or 70, wherein the comparable conditions comprise all of the samples being prepared using the same reagent batch.

72. (previously added) A method of determining both genotype and confidence scores at a genetic locus for a plurality of samples of genetic material wherein the plurality of samples have been prepared under comparable conditions, the method comprising:

(a) assembling reaction-value data points for the samples, each reaction-value data point corresponding to a respective one of the samples and including at least one reaction value;

(b) determining an initial conditional probability for each reaction-value data point for each genotype;

(c) computing a conditional probability of each genotype for each reaction-value data point; and

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(d) determining the genotype and confidence score for each reaction-value data point, thus determining the genotype and confidence score at the genetic locus for each sample.

73. (previously added) A method according to claim 72 wherein each reaction-value data point includes a first reaction value and a second reaction value.

74. (previously added) A method according to claim 73 wherein the first reaction value is indicative of the presence of a first allele at the locus and the second reaction value is indicative of the presence of a second allele at the locus.

75. (previously added) A method of determining the genotype at a locus within genetic material obtained from a biological sample, the method comprising:

A. reacting the material at the locus to produce a first reaction value indicative of the presence of a given allele at the locus;

B. forming a data set including the first reaction value;

C. establishing a distribution set of probability distributions, including at least one distribution, associating hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

D. applying the first reaction value to each pertinent probability distribution to determine a measure of a conditional probability of each genotype of interest at the locus; and

E. determining the genotype based on the data obtained from step (D).

76. (previously added) A method according to claim 75, wherein the distribution set includes a plurality of probability distributions for a corresponding plurality of genotypes of interest.

77. (previously added) A method, according to claim 75, further comprising:

(i) reacting the material at the locus to produce a second reaction value independently indicative of the presence of a second allele at the locus;

(ii) forming a second data set including the second reaction value; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

78. (previously added) A method according to claim 76, further comprising:

(i) reacting the material at the locus to produce a second reaction value;

(ii) applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

79. (previously added) A method according to claim 77, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

80. (previously added) A method according to claim 75, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions;

the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

81. (previously added) A method, according to claim 80, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

(i) performing step (A) with respect to the locus of material obtained from each sample;

(ii) in step (B), including in the data set reaction values obtained from each sample.

82. (previously added) A method according to claim 80, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

(i) performing step (A) at each of the selected loci;

(ii) in step (B), including in the data set reaction values obtained from each of the selected loci.

83. (previously added) A method according to claim 80, wherein step (C) includes:

(i) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(ii) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(iii) using the results of step (ii) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

84. (previously added) A method according to claim 83, wherein step (C) further includes:

(iv) repeating steps (i) through (iii) a desired number of times.

85. (previously added) A method according to claim 75, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data obtained from step (D).

86. (previously added) A method according to claim 80, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data from step (D), the method further comprising:

(F) determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

87. (previously added) A method according to claim 75, wherein each allele is a single specific nucleotide.

88. (previously added) A method according to claim 75, wherein each allele consists of at least two specific nucleotides.

89. (previously added) A method according to claim 75, wherein each allele is defined at least in part by its length in nucleotides.

90. (previously added) A method according to claim 75, wherein each allele is defined by one of the presence and absence of at least one restriction site.

91. (previously added) A method according to claim 78, wherein step (B) includes the step of including in the data set reaction values from prior tests at the locus obtained under comparable conditions.

92. (previously added) A method according to claim 82, wherein the loci are selected on the basis of their ability to discriminate among subjects.

93. (previously added) A method, according to claim 77, wherein the step A' of reacting the material involves using a different reaction from that of step A and the second allele is different from the given allele.

94. (previously added) A method according to claim 75, wherein step (A) includes the step of assaying for the given allele using genetic bit analysis, allele-specific amplification, polymerase chain reaction, or a ligase chain reaction.

95. (previously added) A method according to claim 82, wherein the loci are proximal to one another, so that the set of genotypes so produced may indicate a sequence of nucleotides associated with the genetic material.

96. (New) A method of associating with a sample of genetic material one of a predetermined plurality of genotypic-class identifiers defined with respect to a genetic locus sited in the genetic material together with a corresponding confidence measure, each genotypic-class identifier identifying either a genotype defined with respect to the genetic locus or a failed-experiment condition, each genotype being defined by the identity of one or more alleles defined with respect to the genetic locus, the method comprising the steps of:

(a) carrying out one or more allele-sensitive reactions on the genetic material of the sample at the genetic locus to obtain a plurality of quantitative allele-indicative reaction values, each allele-indicative reaction value being indicative of the likely presence or absence of a particular allele defined with respect to the genetic locus, the plurality of reaction values corresponding to the sample being assembled as a reaction-value data point;

(b) obtaining with respect to each of the genotypic-class identifiers corresponding reaction-value data-point conditional-probability-measure distribution information providing, over a set of hypothetical reaction-value data points, a conditional probability measure as a function of the reaction values of each hypothetical reaction-value data point given the genotypic-class identifier;

(c) evaluating for each of the genotypic-class identifiers the corresponding reaction-value data-point conditional-probability-measure distribution information with respect to the allele-indicative reaction values of the reaction-value data point corresponding to the sample to obtain for each of the corresponding genotypic-class identifiers a reaction-value data-point conditional probability measure of the reaction-value data point given the genotypic-class identifier;

(d) establishing with respect to each genotypic-class identifier a class-identifier conditional probability measure of the genotypic-class identifier given the reaction-value data point corresponding to the sample from the reaction-value data-point conditional probability measure of the reaction-value data point given the genotypic-class identifier to obtain a set of class-identifier conditional probability measures of the respective genotypic-class identifiers given the reaction-value data point;

(e) selecting a highest-probability class-identifier conditional probability measure of a genotypic-class identifier given the reaction-value data point having a highest probability value from the set of class-identifier conditional probabilities to identify a most-likely genotypic-class identifier corresponding to said highest-probability class-identifier conditional probability measure for association with the sample; and

(f) establishing a confidence measure for the association of the most-likely genotypic-class identifier with the sample, the confidence measure being established from

values of the class-identifier conditional probability measures of the respective genotypic-class identifiers given the reaction-value data point corresponding to the sample.

97. (New) The method according to claim 96 in which at least one genotypic-class identifier identifies a failed-experiment condition.

98. (New) The method according to claim 96 in which the confidence measure is an LOD score.

99. (New) The method according to claim 96 in which the allele-indicative reaction values are measurements of an optical signal or a digital image intensity value.

100. (New) The method according to claim 96 in which the allele-indicative reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, hybridization, allele-specific amplification and a ligase chain reaction.

101. (New) The method according to claim 100 in which the allele-indicative reaction values are obtained by assaying for alleles using genetic bit analysis.

102. (New) The method according to claim 96, further comprising the step of triggering an alarm condition upon detecting a statistically significant downward trend in confidence scores over time.

103. (New) The method according to claim 96 in which the allele-indicative reaction values are obtained by assaying for one or more alleles that provide information relating to a trait.

104. (New) The method according to claim 96 in which the allele-indicative reaction values are obtained by assaying for one or more alleles that provide information pertaining to parentage of a subject.

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105. (New) The method according to claim 96 in which the allele-indicative reaction values are obtained by assaying for one or more alleles that provide information useful for determining the identity of a subject.